

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2002, 03:41:53 ; Search time 1909.32 Seconds  
(without alignments)  
24735.349 Million cell updates/sec

Title: US-09-652-292-1

Perfect score: 4395

Sequence: 1 gagggggtcttcgcaggcc.....attatttgaataaaaaaaa 4395

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_htc:*
10: gb_est1:*
11: gb_est2:*
12: gb_htc:*
13: gb_gss:*
14: em_gas_fun:*
15: em_gas_hum:*
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17: em_gas_pln:*
18: em_gas_pro:*
19: em_gas_rod:*
20: em_gas_vrt:*
21: em_gas_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	13.2	678	13	AQ037826 CIT-HSP-2
2	576	13.1	580	10	AA628914 af28a03.s
3	478	10.9	479	10	AL449907
4	477	10.9	528	10	AA404352
5	466	10.6	466	10	AL449914
6	465	10.6	481	10	AL449906
7	460	10.5	461	10	AL449913
8	454	10.3	454	10	AI334230 qq09h04.x
9	449	10.2	563	10	AI042706
10	408	9.3	459	10	AL449887
11	404	9.2	532	10	AI041537
12	384	8.7	859	11	BG563879 602584689

13	378	8.6	450	10	AL449886
14	377	8.6	475	10	AL449910
15	366	8.3	685	11	BG568246
16	364	8.3	425	10	AA134031
17	364	8.3	1049	11	BF688799
18	354	8.1	456	10	AA115737
19	351	8.0	910	10	AL554162
20	344	7.8	363	10	AL449889
21	335	7.6	706	11	BG566556
22	320	7.3	368	11	C04258
23	310	7.1	467	10	AA403072
24	290	6.6	341	10	AL449890
25	289	6.6	925	11	BG569139
26	283	6.4	402	10	AL449905
27	283	6.4	453	10	AA133497
28	279	6.3	624	11	W02942
29	275	6.3	342	11	W31922
30	271	6.2	450	10	AI081145
31	269	6.1	495	10	AA007343
32	263	6.0	330	10	AI289525
33	260	5.9	396	10	AL449904
34	259	5.9	431	10	AI097288
35	238	5.4	358	11	W38959
36	234	5.3	372	10	AI088144
37	227	5.2	235	10	AL449622
38	219	5.0	405	10	AI753932
39	216	4.9	454	10	AI753293
40	207	4.7	318	10	AI753418
41	207	4.7	354	10	AI277131
42	207	4.7	561	10	AA133966
43	206	4.7	306	10	AA313045
44	206	4.7	523	10	AW298226
45	199	4.5	242	10	AL449623

#### ALIGNMENTS

#### RESULT

AQ037826 678 bp DNA 11-JUL-1998  
CIT-HSP-2326P11.TF CIT-HSP Homo sapiens genomic clone 2326P11, DNA sequence.  
ACCESSION AQ037826  
VERSION AQ037826.1 GI:3303658  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 678)  
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.  
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)  
JOURNAL Unpublished (1998)  
COMMENT Other\_GSSs: CIT-HSP-2326P11.TR  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC end search page:  
http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13-21  
Class: BAC ends.  
Location/Qualifiers  
1..678  
/organism="Homo sapiens"



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Qy 4117 aaaaaaaaaatttaacaaataattctgtgaagaatcaattggcgtatatgggaatttagga 4176
Db 100 AAAAAAAAAAATTAACAAAATATTCTGTGAAGATCAATTGGCTATATGGAATTTAGGA 41
Qy 4177 taagaataattcaataaagaataattttacaataaa 4212
Db 40 TAAAGAATATTACAAATAAAGAAATATTACAAATAAA 5

RESULT 3
AL449907/c 479 bp mRNA EST 15-NOV-2000
LOCUS AL449907 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
DEFINITION mRNA sequence.
ACCESSION AL449907
VERSION AL449907.1 GI:11181532
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 479)
AUTHORS Stavrides,G.S., Huckle,E.J. and Deloukas,P.
TITLE Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
JOURNAL Unpublished (2000)
COMMENT Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerv@sanger.ac.uk
Sanger Centre name : sccd3097.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrides GS)"
/tissue_type="Lung"
/dev_stage="fetal"
/notes="cDNA fragment isolated using a cDNA end rescue
technique"
BASE COUNT 137 a 126 c 109 g 107 t
ORIGIN
Query Match 10.9% Score 478; DB 10; Length 479;
Best Local Similarity 100.0%; Pred. No. 8.2e-174; Indels 0; Gaps 0;
Matches 478; Conservative 0; Mismatches 0;

Qy 2705 ttggctcgtcgttcattcgtgtaggaatgaccacggcctcagttcccccatttgat 2764
Db 478 TTGGTCTGCTGCTGTCATTGCTGTAGGAATGACACGGGCTCAGTTCCCCATTGTAT 419
Qy 2765 aatggaagcctgtaccaggtcattcttaagattctcctgactcagtgagctgaatt 2824
Db 418 AATGGGAAGCCTGTACCAGGTCATTCTTAAGATTCTCTGACTCCAGTGAGCTGAATT 359
Qy 2825 ctataatcgtcgtcgttaggagctgtctcaggatggtgcaggatggtcttcggaagagga 2884
Db 358 CTAAATGCTGGTCTAGGAGCTGTCTCCAGGATGTTGTCAGGATGGCTTTGCGGAAGGAGA 299
Qy 2885 tgggttggagggccaaacacctcgtcgtcgaattccttcctcctccttggcagcccttg 2944
Db 298 TGGGTTTGGAGGGCAACAACCTCCTGTGTCATATGTCCTTTGGCTTTGGCGACCCCTTG 239
Qy 2945 aacttgagtaataaacaactccctgaacctcagttctcctcactcgtcagaaatgggataat 3004
Db 238 AACTTGAGTAATAAACAACTCCCTGAACCTCAGTTCTCTCATCTCGAGAAATGGGGATAAT 179
Qy 3005 tatgtcccccgggttatattagaccctcgtttccttcaggagggtcccccagctggtccag 3064
Db 178 TATGTCCCGGGGTATATTAGACCCCTGTTTCCTTTCAGGAGGGTCCCGACGCTGGTCCAG 119

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Qy 3065 ggccctgggaatttctactatctcattaccagggtccctcttggaccctgtaaagg 3124
Db 118 GGCCCTGGGAATTTCTACTTATCTCTATTACCCAGGTCCTCTTTGGACCCCTGTAAAGG 59
Qy 3125 gtcagggtgaatcagatcggggagctgagcaagtagctatgactgcagatcatcgttaagg 3182
Db 58 GTCAGGGTGAATCAGATGGGGGACTGACCAAGTAGCTATGACTGCGAGATCATGTAAGG 1

RESULT 4
AA404352/c 528 bp mRNA EST 16-MAY-1997
LOCUS AA404352 Soares_total_fetus_NB2HF8_9w Homo sapiens cDNA clone
DEFINITION IMAGE:758347 3', mRNA sequence.
ACCESSION AA404352
VERSION AA404352.1 GI:2059077
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 528)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Giesel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
T., Waterston,R. and Wilson,R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 464.
FEATURES
Location/Qualifiers
1..528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Soares_total_fetus_NB2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/notes="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGCTTAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 181 a 77 c 75 g 195 t
ORIGIN
Query Match 10.9% Score 477; DB 10; Length 528;
Best Local Similarity 99.8%; Pred. No. 1.9e-173;
Matches 527; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3865 ttgaacactgtcattccgctttcagctgacagctgcacaaatcatttaagagggtctga 3924
Db 528 TTGAACACTGTCATCCGTTTCAGCTGACAGCTGCTCAATCATCTTTAAGAGGAGTCTGA 469
Qy 3925 catctatttcatgttttacttttcttctcactagtgtaaacacaaatttcaacca 3984
Db 468 CATTCATTTTCATTTGTTTACTTTTGTCTCTACTACTAGTAAACAAAATTTCAACCA 409
Qy 3985 goattcatgcccgaacctatatacccatcttctcagtgctcagtgctacagtggttatt 4044

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Db 408 GCATTTCATGCGGAACCTATACCCATTCTTCAGTGCTAGCTACAGTATATACAGGATTT 349
QY 4045 ttattcgtagcttaattttgcaaatcatcgtgccaatcgcagctgtagttagctttggat 4104
Db 348 TTAFTCTGAGTCTAATTTTGTCAAAATCATGCGCAATCGCACTGATAGTTGAGT 289
QY 4105 acaaggttggcaaaaaaataatttaacaaaatattctctgtaagaatcaattggctata 4164
Db 288 ACAAGGTTGGCAAAAAAATAATTAACAAAATATTCTGTGAAGAAATCAATTTGGCTATA 229
QY 4165 tggaaattaggataaagaataatttacaataaagaataatttacaataaagaagattattatt 4224
Db 228 TGGAAATTTAGGATAAAGAAATATTACAAATAAAGAAATATTACAAATAAAGAGTTTATTATT 169
QY 4225 atttgaagttggtgcaacaaacataccctttatctctgtataaatttatcacacacaaaa 4284
Db 168 ATTGTGAAGTTGTGACCAACAAACATACCCCTTTATCTCTGTGTAATAATTTATACACACAAA 109
QY 4285 attaacaagaattctgaagaattatttggtctatatggaatttaggataagaattttac 4344
Db 108 ATTACAAAGATTTCTGAAGAATTAATTGGCTATATGGAATTTAGGATAGAAATATTATAC 49
QY 4345 aataagagratattacaataaagaagttgttattattttgtaaaaaaa 4392
Db 48 AATAAGAGTATTACAAATAAAGAGTTGTATTATTATTGTAAAAAAA 1

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RESULT 5
AL449914/c
LOCUS AL449914 466 bp mRNA EST 15-NOV-2000
DEFINITION AL449914 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
mRNA sequence.
ACCESSION AL449914
VERSION AL449914.1 GI:11181539
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 466)
AUTHORS Stavrides,G.S., Huckle,E.J. and Deloukas,P.
TITLE Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P.
JOURNAL Unpublished (2000)
COMMENT Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name : scc3335.
FEATURES
Location/Qualifiers
1..466
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrides GS)"
/tissue_type="lung"
/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue
technique"
BASE COUNT 117 a 149 c 141 g 59 t
ORIGIN

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Query Match 10.6%; Score 466; DB 10; Length 466;
Best Local Similarity 100.0%; Pred. No. 3.6e-169;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 309 gaccttggattgaactggcagctaatcagctgacctgctgacctgacctgacctgacct 368
Db 466 GACCTTGGTTATGAACCTGCACCTCATATCAGGTGCGCTGCTGCACCTGCAGTTGACTT 407
QY 369 tgggctaagctgcttggagcaggagttcctgtggtggcagcctgctcctgggggctcct 428

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Db 406 TGGGCTAAGCTGTTGGAGCAGAGTTCTGGTGGGAGGCTGCTCTCTGGGGGCTCTCCT 347
QY 429 cgcctcccttggttggtggttctctcattgactgctatggcaggaagcaagcctcctcgg 488
Db 346 CGCCTCCCTGGTTGGTGGCTTCTCTCAATTGACTGCTATGGCAGGAAGCAAGCCATCTCTGG 287
QY 489 gagcaacttggtgctgctgagcaggcagcctgacctgggctgggctgggttccctggcctg 548
Db 286 GAGCAACTTGGTGGCTGCTGGCAGGAGCAGCCTGACCCCTGGGCTGGCTGGTTCCTGGGCTG 227
QY 549 gctgtcctggggccgcgcctggttggttggcttccatttccctcctcctcctcctgctg 608
Db 226 GCTGGTCTGGGCGCGCTGCTGGTGGCTTCGCCATTTCCCTCTCCCAATGGCTTGGCTG 167
QY 609 tatctagctgctagagctggtggggccacggcagcgggagtgctggtgctcctctatga 668
Db 166 TATCTAGCTGTCTAGAGCTGGTGGGCGCCACGGCAGCGGGGAGTCTGTGTCTCTCTATGA 107
QY 669 ggcagcgcacacctgggcatcctgctctcctcctcctcctcctcctcctcctcctgctg 728
Db 106 GGCAGGCATCACCCTGGGCATCCTCTCTCTCTATGCCCCCTCAACTATGCATGCTGCTGCTAC 47
QY 729 ccctggggatggaggcacatgttcggtgggacctgacctgacctgct 774
Db 46 CCCCTGGGGATGGAGGACATGTTGGGCTGGGCCACTGCACCTGCT 1

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RESULT 6
AL449906
LOCUS AL449906 481 bp mRNA EST 15-NOV-2000
DEFINITION AL449906 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
mRNA sequence.
ACCESSION AL449906
VERSION AL449906.1 GI:11181531
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 481)
AUTHORS Stavrides,G.S., Huckle,E.J. and Deloukas,P.
TITLE Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P.
JOURNAL Unpublished (2000)
COMMENT Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name : scc3096.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrides GS)"
/tissue_type="lung"
/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue
technique"
BASE COUNT 114 a 114 c 124 g 127 t 2 others
ORIGIN

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Query Match 10.6%; Score 465; DB 10; Length 481;
Best Local Similarity 100.0%; Pred. No. 8.5e-169;
Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2729 aggaatgaccacggcctcagcttccctcctcctcctcctcctcctcctcctcctcct 2788
Db 1 AGGAATGACCACGGGCGCTCAGTTTCCCATTTGTATATATGGAAGCCTGTACCAGTCAAT 60
QY 2789 tcttaagatttctcctgactcagctgagctggaattctaaatgctggttagagagctgctc 2848
Db 61 TCTTAAGATTCTCCTGACCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 120

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Qy	456	tgactgctatgacaggaagaacccactctcctggagcaacttgctgctgctgacaggcaag	515
Db	121	TGACTGCTATGCGAGGAAGCAAGCCATCTCTGGGAGCAACTTGTGTCTGTCTGGCAGGCAG	180
Qy	516	cctgaccctggccctgctggtttccctcctggcctggctggtcctgggcccgcctcgttgttg	575
Db	181	CCTGACCCTGGCCCTGGCTGGTTCCCTGGCCCTGGCTGGTCTCTGGGCCGCGCTGTGGTTGG	240
Qy	576	cttggccattccctcctccctcctggctgctgctgatactagctgtcagagctggttggggccc	635
Db	241	CTTCGCCATTCCCTCTCCTCCATGGCTTGCTGTATCTACGTGTGACAGCTGGTGGGGCC	300
Qy	636	acggcagcggggagtgtggtgtccctcctatgagggcaggcatcacctggggcatcctgct	695
Db	301	ACGGCAGCGGGAGTGCTGGTGTCCCTCTATGAGGCAGGCATCACCGTGGGCATCCTGTCT	360
Qy	696	ctcctatgcccctcaactatgcactggtcgtgtacccccctggggatggaggacatgttcgg	755
Db	361	CTCCTATGCCCTCAACTATGCACTGGCTGTGTACCCCTGGGGATGGAGGCACATGTTCCG	420
Qy	756	ctgggccactgcaactgctgtctctgcaatccctcagcctc	795
Db	421	CTGGGCCACTGACCTGCTGTCTCTGCAATCCCTCAGCTC	460

RESULT	8
AC1334230/c	
LOCUS	A1334230 454 bp mRNA
DEFINITION	EST 13-FEB-1999 gg09h04.x1 Soares_NhhMPU_S1 Homo sapiens cDNA clone IMAGE:1932055 3', mRNA sequence.
ACCESSION	A1334230
VERSION	A1334230.1 GI:4070789
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 454) NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/holgap">http://www.ncbi.nlm.nih.gov/holgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP). Tumor Gene Index Unpublished (1997)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. Insert Length: 599 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 409.
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FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:1932035"
/clone_lib="Soares_NHHMPu_S1"
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pregnant uterus"
/lab_host="DH10B"
/notes="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NBHPU, and fetal heart NBHH19W) were mixed, and as circ
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools
5,000 clones made from the same 3 libraries. The pools
consisted of 1.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
128 a 112 c 97 g 117 t
BASE COUNT
ORIGIN

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Site-2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBH, pregnant uterus NBHpu, and fetal heart NBHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."



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ACCESSION AL449887
VERSION AL449887.1 GI:11181512
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE Stavrides,G.S., Huckle,E.J. and Deloukas,P.
JOURNAL Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P.
COMMENT Unpublished (2000)
Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : sccdl338.
FEATURES
source
1. .459
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrides GS)"
/tissue_type="Lung"
/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue
technique"
BASE COUNT 74 a 148 c 142 g 95 t
ORIGIN
Query Match 9.3%; Score 408; DB 10; Length 459;
Best Local Similarity 99.8%; Pred. No. 8.4e-147;
Matches 458; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 733 tgggatgagggcacatgttcgctggcgcactgcacgtgctgtcgtcaatccctcagc 792
Db 1 TGGGATGAGGACATGTCGGCTGGCCACTGCACCTGCTGTCTGCTGCAATCCCTCAGC 60
Qy 793 etcccttctcctcctgctgtacagatgagactgagactgacacacacacagacatccacac 852
Db 61 CTCCTCTTCTCCCTGCTGTACAGATGAGACTGCAACACACACAGGACCTCATCCCACTC 120
Qy 853 caggaggtgagggcccccagctgggcccggggagggccagctactcctttctggacctc 912
Db 121 CAGGGAGGTGAGGCCCCCAAGCTGGGCCCGGGAGGCCACGCTACTCTTCTGGACCTC 180
Qy 913 ttcagggcagcgataacatgcgagggccgggacacagtgggcctgggctggtgctcttc 972
Db 181 TTCAGGGCAGCGGATAACATGCGAGGCGCGGACACAGTGGGCTGGGCTGGCTCTTC 240
Qy 973 cagcaactaacaggcagccacgctgctgtgctgctgctgctgctgctgctgctgctgct 1032
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AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabps@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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High quality sequence stop: 444.
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1. .532
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was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 181 a 79 c 78 g 194 t
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[illegible]



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Db	202	GATGAGACTGCAACACACAAAGGACCTCATCCCACTCCAGGAGGTGAGGCCCCCAAGCTG	261	
Qy	877	ggcccgggagggccaggtactcctcttgagacctcttcaggggcacgcgataacatgcga	936	
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Db	322	GGCCGGACACAGTGGGCCTGGGCTGTGTCTTCCAGCAACTAACAGGGCAGCCCAAC	381	
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AUTHORS	1 (bases 1 to 475)			
TITLE	Stavrides,G.S., Huckle,E.J. and Deloukas,P.			
JOURNAL	Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P			
COMMENT	Unpublished (2000) Contact: Stavrides GS The Sanger Centre Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK Email: humquerv@sanger.ac.uk Sanger Centre name : sccd3101.			
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Qy	2688	ggcctcagttctagtccttggctgctgggtgctcattgctgtaggaaatgaccacgggcctc	2747
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Qy	2748	agtttcccaatttgtataaatggaagcctgtaccaggtcattcttaagaatttctctgcac	2807
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Qy	2808	tccagtgagctggaattctaaatgctggtctagtagagctgtctccaggatggtgacagatg	2867
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